

RAW SEQUENCE LISTING

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Application Serial Number: 10/595,858
Source: IFWO
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RAW SEQUENCE LISTING

DATE: 06/02/2006

PATENT APPLICATION: US/10/595,858

TIME: 09:22:00

Input Set : A:\Sequence Listing to File.TXT
 Output Set: N:\CRF4\06022006\J595858.raw

3 <110> APPLICANT: YOSHINAGA, Takashi
 4 ARAI, Toru
 6 <120> TITLE OF INVENTION: hERG channel-expressing cell
 8 <130> FILE REFERENCE: 09857/0204372-US0
 10 <140> CURRENT APPLICATION NUMBER: 10/595,858
 11 <141> CURRENT FILING DATE: 2006-05-16
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/017441
 14 <151> PRIOR FILING DATE: 2004-11-17
 16 <150> PRIOR APPLICATION NUMBER: JP 2003-387255
 17 <151> PRIOR FILING DATE: 2003-11-17
 19 <160> NUMBER OF SEQ ID NOS: 13
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 4070
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo Sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (184)..(3660)
 33 <400> SEQUENCE: 1
 34 acgcggcctg ctcaggcctc cagcggccgg tcggagggga ggccggagggc gagcggaggac 60
 36 cccgcggccgc agtccagtct gtgcgcgcctt ggcgcgggtgc gggaccagcg 120
 38 cccggccaccc gaagccatgt gcgtcgccgg gtgggtgggc ccgcggccggcg ccatgggctc 180
 40 agg atg ccg gtg cgg agg ggc cac gtc gcg ccg cag aac acc ttc ctg 228
 41 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu
 42 1 5 10 15
 44 gac acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc 276
 45 Asp Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile
 46 20 25 30
 48 gcc aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc 324
 49 Ala Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly
 50 35 40 45
 52 ttc tgc gag ctg tgc ggc tac tcg cgg gcc gag gtg atg cag cga ccc 372
 53 Phe Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro
 54 50 55 60
 56 tgc acc tgc gac ttc ctg cac ggg ccc cgc acg cag cgc cgc gct gcc 420
 57 Cys Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala
 58 65 70 75
 60 gcg cag atc gcg cag gca ctg ctg ggc gcc gag gag cgc aaa gtg gaa 468
 61 Ala Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu
 62 80 85 90 95
 64 atc gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat 516
 65 Ile Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp

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66	100	105	110																
68	gtg	gtg	ccc	gtg	aag	aac	gag	gat	ggg	gct	gtc	atc	atc	atc	ctc		564		
69	Val	Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	Ala	Val	Ile	Met	Phe	Ile	Leu			
70																			
72	aat	ttc	gag	gtg	gtg	atg	gag	aag	gac	atg	gtg	ggg	tcc	ccg	gct	cat		612	
73	Asn	Phe	Glu	Val	Val	Met	Glu	Lys	Asp	Met	Val	Gly	Ser	Pro	Ala	His			
74																			
76	gac	acc	aac	cac	cg	ggc	ccc	ccc	acc	agc	tgg	ctg	gcc	cca	ggc	cg		660	
77	Asp	Thr	Asn	His	Arg	Gly	Pro	Pro	Thr	Ser	Trp	Leu	Ala	Pro	Gly	Arg			
78																			
80	gcc	aag	acc	ttc	cgc	ctg	aag	ctg	ccc	g	ctg	ctg	g	ctg	acg	gcc		708	
81	Ala	Lys	Thr	Phe	Arg	Leu	Lys	Leu	Pro	Ala	Leu	Leu	Ala	Leu	Thr	Ala			
82																			
84	cgg	gag	tcg	tcg	gtg	cg	tcg	ggc	ggc	g	ggc	ggc	g	ggc	ggc	ccg		756	
85	Arg	Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Pro			
86																			
88	ggg	gcc	gtg	gtg	gtg	gac	gtg	gac	ctg	acg	ccc	g	ca	ccc	agc	agc		804	
89	Gly	Ala	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser	Ser				
90																			
92	gag	tcg	ctg	ggc	ctg	gac	gaa	gtg	aca	g	cc	atg	gac	aac	cac	gtg	gca		852
93	Glu	Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val	Ala			
94																			
96	ggg	ctc	ggg	ccc	g	cg	gag	gg	cg	gt	gg	ctg	gt	gg	ccc	gg	tct		900
97	Gly	Leu	Gly	Pro	Ala	Glu	Gly	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly	Ser			
98																			
100	ccg	ccc	ccg	agc	gc	ccc	gg	cc	ag	ctc	cc	tc	cc	cc	gg	gg	cac		948
101	Pro	Pro	Arg	Ser	Ala	Pro	Gly	Gln	Leu	Pro	Ser	Pro	Arg	Ala	His	Ser			
102																			
104	ctc	aac	ccc	gac	gg	tc	gg	tcc	agc	tgc	agc	ctg	gg	cc	gg	ac	cg		996
105	Leu	Asn	Pro	Asp	Ala	Ser	Gly	Ser	Ser	Cys	Ser	Leu	Ala	Arg	Thr	Arg			
106																			
108	tcc	cga	gaa	agc	tgc	gg	agc	gt	cg	cg	gg	cc	tc	gg	cc	gac	gac		1044
109	Ser	Arg	Glu	Ser	Cys	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	Asp	Asp			
110																			
112	atc	gag	gg	atg	cg	gg	gg	gt	ctg	cc		1092							
113	Ile	Glu	Ala	Met	Arg	Ala	Gly	Val	Leu	Pro	Pro	Pro	Pro	Arg	His	Ala			
114																			
116	agc	acc	ggg	gg	atg	cac	cc	ctg	cg	agc	gg	ttg	ctc	aa	tcc	acc			1140
117	Ser	Thr	Gly	Ala	Met	His	Pro	Leu	Arg	Ser	Gly	Leu	Leu	Asn	Ser	Thr			
118																			
120	tcg	gac	tcc	gac	ctc	gt	cg	tac	cg	acc	att	agc	aag	att	ccc	caa			1188
121	Ser	Asp	Ser	Asp	Leu	Val	Arg	Tyr	Arg	Thr	Ile	Ser	Lys	Ile	Pro	Gln			
122																			
124	atc	acc	ctc	aa	ttt	gt	gac	ctc	aa	gg	gac	cc	ttc	ttg	gt	tcg			1236
125	Ile	Thr	Leu	Asn	Phe	Val	Asp	Leu	Lys	Gly	Asp	Pro	Phe	Leu	Ala	Ser			
126																			
128	ccc	acc	agt	gac	cgt	gag	atc	ata	gca	cct	aag	ata	aag	gag	cga	acc			1284
129	Pro	Thr	Ser	Asp	Arg	Glu	Ile	Ile	Ala	Pro	Lys	Ile	Lys	Glu	Arg	Thr			
130																			

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132 cac aat gtc act gag aag gtc acc cag gtc ctg tcc ctg ggc gcc gac	1332
133 His Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp	
134 370 375 380	
136 gtc ctg cct gag tac aag ctg cag gca ccg cgc atc cac cgc tgg acc	1380
137 Val Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr	
138 385 390 395	
140 atc ctg cat tac agc ccc ttc aag gcc gtc tgg gac tgg ctc atc ctg	1428
141 Ile Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu	
142 400 405 410 415	
144 ctg ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc ttc	1476
145 Leu Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe	
146 420 425 430	
148 ctg ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc tac	1524
149 Leu Leu Lys Glu Thr Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr	
150 435 440 445	
152 gcc tgc cag ccg ctg gct gtc gtc gac ctc atc gtg gac atc atg ttc	1572
153 Ala Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe	
154 450 455 460	
156 att gtc gac atc ctc atc aac ttc cgc acc acc tac gtc aat gcc aac	1620
157 Ile Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn	
158 465 470 475	
160 gag gag gtc agc cac ccc ggc ccg atc gcc gtc cac tac ttc aag	1668
161 Glu Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys	
162 480 485 490 495	
164 ggc tgg ttc ctc atc gac atg gtc gcc gcc atc ccc ttc gac ctg ctc	1716
165 Gly Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu	
166 500 505 510	
168 atc ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act gcg	1764
169 Ile Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala	
170 515 520 525	
172 cgg ctg ctg cgg ctg gtc cgc gtc gcg ccg aag ctg gat cgc tac tca	1812
173 Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser	
174 530 535 540	
176 gag tac ggc gcg gcc gtc ttc ttg ctc atg tgc acc ttt gcg ctc	1860
177 Glu Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu	
178 545 550 555	
180 atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg gag	1908
181 Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu	
182 560 565 570 575	
184 cag cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc gac	1956
185 Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp	
186 580 585 590	
188 cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc atc	2004
189 Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile	
190 595 600 605	
192 aag gac aag tat gtc acg gcg ctc tac ttc acc ttc agc agc ctc acc	2052
193 Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr	
194 610 615 620	
196 agt gtc ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag atc	2100

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197 Ser Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile		
198 625 630 635		
200 ttc tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc atc	2148	
201 Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile		
202 640 645 650 655		
204 ttc ggc aac gtg tcg gcc atc atc cag cgg ctg tac tcg ggc aca gcc	2196	
205 Phe Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala		
206 660 665 670		
208 cgc tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc cac	2244	
209 Arg Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His		
210 675 680 685		
212 cag atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag cac	2292	
213 Gln Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Tyr Phe Gln His		
214 690 695 700		
216 gcc tgg tcc tac acc aac ggc atc gac atg aac gcg gtg ctg aag ggc	2340	
217 Ala Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly		
218 705 710 715		
220 ttc cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc tca	2388	
221 Phe Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser		
222 720 725 730 735		
224 ctg ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc ctt	2436	
225 Leu Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu		
226 740 745 750		
228 cgg gcc ctg gcc atg aag ttc aag acc aca cat gca ccg cca ggg gac	2484	
229 Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp		
230 755 760 765		
232 aca ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc tcc	2532	
233 Thr Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser		
234 770 775 780		
236 cgg ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc ctg	2580	
237 Arg Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu		
238 785 790 795		
240 ggg aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg cct	2628	
241 Gly Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro		
242 800 805 810 815		
244 ggc aag tcg aac ggg gat gtg cgg gcc ctc acc tac tgt gac cta cac	2676	
245 Gly Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His		
246 820 825 830		
248 aag atc cat cgg gac gac ctg ctg gag gtg ctg gac atg tac cct gag	2724	
249 Lys Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu		
250 835 840 845		
252 ttc tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg cga	2772	
253 Phe Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg		
254 850 855 860		
256 gat acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag ggt	2820	
257 Asp Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly		
258 865 870 875		
260 ggc ttc agt cgg caa cgc aag cgc aag ttg tcc ttc cgc agg cgc acg	2868	
261 Gly Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr		

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262	880	885	890	895	
264	gac aag gac acg gag cag cca ggg gag gtg tcg gcc ttg ggg ccg ggc				2916
265	Asp Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly				
266	900	905	910		
268	cgg gcg ggg gca ggg ccg agt agc cgg ggc cgg ccg ggg ggg ccg tgg				2964
269	Arg Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp				
270	915	920	925		
272	ggg gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag gat				3012
273	Gly Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp				
274	930	935	940		
276	gag ggc cca ggc cgc agc tcc agc ccc ctc cgc ctg gtg ccc ttc tcc				3060
277	Glu Gly Pro Gly Arg Ser Ser Pro Leu Arg Leu Val Pro Phe Ser				
278	945	950	955		
280	agc ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg gag				3108
281	Ser Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu				
282	960	965	970	975	
284	gac tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc ttc				3156
285	Asp Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe				
286	980	985	990		
288	tca gga gtg tcc aac att ttc agc ttc tgg ggg gac agt cgg ggc cgc				3204
289	Ser Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg				
290	995	1000	1005		
292	cag tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc				3249
293	Gln Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu				
294	1010	1015	1020		
296	ctc aac atc ccc ctc tcc agc ccg ggt cgg cgg ccc cgg ggc gac				3294
297	Leu Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp				
298	1025	1030	1035		
300	gtg gag agc agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg				3339
301	Val Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu				
302	1040	1045	1050		
304	gag acc cgg ctg agt gca gac atg gcc act gtc ctg cag ctg cta				3384
305	Glu Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu				
306	1055	1060	1065		
308	cag agg cag atg acg ctg gtc ccg ccc gcc tac agt gct gtg acc				3429
309	Gln Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr				
310	1070	1075	1080		
312	acc ccg ggg cct ggc ccc act tcc aca tcc ccg ctg ttg ccc gtc				3474
313	Thr Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val				
314	1085	1090	1095		
316	agc ccc ctc ccc acc ctc acc ttg gac tcg ctt tct cag gtt tcc				3519
317	Ser Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser				
318	1100	1105	1110		
320	cag ttc atg gcg tgt gag gag ctg ccc ccg ggg gcc cca gag ctt				3564
321	Gln Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu				
322	1115	1120	1125		
324	ccc caa gaa ggc ccc aca cga cgc ctc tcc cta ccg ggc cag ctg				3609
325	Pro Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu				
326	1130	1135	1140		

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12

VERIFICATION SUMMARY

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